

Serial Number: 09854731

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/854,731

DATE: 06/12/2001

TIME: 11:45:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\06112001\I854731.raw

See p. 5

```

3 <110> APPLICANT: Allen, Steve
4   Lee, Jian Ming
6 <120> TITLE OF INVENTION: Plant Protein Kinases
8 <130> FILE REFERENCE: BB-1171
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/854,731
C--> 11 <141> CURRENT FILING DATE: 2001-05-14
13 <150> PRIOR APPLICATION NUMBER: 60/092,438
W--> 14 <151> PRIOR FILING DATE: July 10, 1998
16 <160> NUMBER OF SEQ ID NOS: 23
18 <170> SOFTWARE: Microsoft Office 97
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 484
22 <212> TYPE: DNA
23 <213> ORGANISM: Zea mays
25 <220> FEATURE:
26 <221> NAME/KEY: unsure /
27 <222> LOCATION: (389)
29 <220> FEATURE:
30 <221> NAME/KEY: unsure /
31 <222> LOCATION: (396)
33 <220> FEATURE:
34 <221> NAME/KEY: unsure /
35 <222> LOCATION: (402) /
37 <220> FEATURE:
38 <221> NAME/KEY: unsure /
39 <222> LOCATION: (430)
41 <220> FEATURE:
42 <221> NAME/KEY: unsure /
43 <222> LOCATION: (467)
45 <220> FEATURE:
46 <221> NAME/KEY: unsure /
47 <222> LOCATION: (469)
49 <220> FEATURE:
50 <221> NAME/KEY: unsure /
51 <222> LOCATION: (479)
53 <400> SEQUENCE: 1
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55 aaggcgccgc cgggtgaagcg cgtgtccagc gccgggctgc tggtcggctc ggtgctcaag 120
56 cgcaggacgg agaaccttaa ggacaagtac agcctggggc ggcgcctcgg gcagggccag 180
57 ttcggcacca cgtacctgtg cgtggagcgg gccacgggca aggagttcgc gtgcaagtcc 240
58 atcctgaagc gcaactcgtc accgacgacg acgtggagga cgtccgccgg gagatccaga 300
59 taatgcacca cctggcgggc caccccaacg tgatctccat ccgcggcgcc tacgaggacg 360
W--> 60 ccgtcgccgt gacctcgtca tggactctng gccgcngcga antgttcaag gatgtgcaga 420
W--> 61 agggcactan acgagagaag gccgcgagct cgcaggatat tcgcgtntna ggcgtgcant 480
62 catg
64 <210> SEQ ID NO: 2
65 <211> LENGTH: 101

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66 <212> TYPE: PRT
67 <213> ORGANISM: Zea mays
69 <220> FEATURE: /
70 <221> NAME/KEY: UNSURE
71 <222> LOCATION: (62)
73 <400> SEQUENCE: 2
74 Pro Pro Val Lys Arg Val Ser Ser Ala Gly Leu Leu Val Gly Ser Val
75   1           5           10           15
77 Leu Lys Arg Arg Thr Glu Asn Leu Lys Asp Lys Tyr Ser Leu Gly Arg
78           20           25           30
80 Arg Leu Gly Gln Gly Gln Phe Gly Thr Thr Tyr Leu Cys Val Glu Arg
81           35           40           45
W--> 83 Ala Thr Gly Lys Glu Phe Ala Cys Lys Ser Ile Leu Lys Xaa Leu Val
84           50           55           60
86 Thr Asp Asp Asp Val Glu Asp Val Arg Arg Glu Ile Gln Ile Met His
87 65           70           75           80
89 His Leu Ala Gly His Pro Asn Val Ile Ser Ile Arg Gly Ala Tyr Glu
90           85           90           95
92 Asp Ala Val Ala Val
93           100
95 <210> SEQ ID NO: 3
96 <211> LENGTH: 2374
97 <212> TYPE: DNA
98 <213> ORGANISM: Oryza sativa
100 <400> SEQUENCE: 3
101 gcacgagggc gtattccgat ttctctctct ctctcctctt cttcttcttc ttcttcccca 60
102 acgagcgact cgcctccacc tcctcgacct ccacctcgcg aggcggcggt gcggggggcc 120
103 ccaaacccta accctaattc cgctgcgccc gcgcccgcgc ccgcgcgcgc cgacaggctg 180
104 ttgttgttgt tgccatgggg cagtgtctac gcaagggcgc gtcggggagg acggcggaag 240
105 atgagggcgg ggtggtgacg gagcaccagt cgccgcgcgc ggcgaacggg ctgccgtcga 300
106 cgccgcgcgc gcagcaggcg caggcgagg cgagcagggt ggggacgcgc aggcggcggt 360
107 ggagtaagtc cggatcgacg acgcccgggc accagacgcc tgggggtggc tggccgagcc 420
108 cgtaccgctc cgggggcgcg agcccgcctc cggccggggg gtcgccgtcg ccggcgagg 480
109 cgacgcccag gaggttcttc aagcggccgt tcccgcgcgc gtcgccggcc aagcacataa 540
110 aggccacgct cgccaagagg ctgggtgggg ggaagcccaa ggaagggacg ataccggagg 600
111 agggaggcgt gggcgctggc ggcggcggtg gaggggccgc ggatggggcg gagacggaga 660
112 ggccattgga caagacgttc gggttctcga agaacttcg cgcaagtac gagctcggga 720
113 agggaggtgg gaggggccac ttcggacaca cttgctccgc cgtcgtcaag aaggcgagt 780
114 acaagggaca gaccgtcgcc gtcaagatca tcgccaaagc taagatgaca acggcaatat 840
115 ccattgagga tgttcgtaga gaagtaaaaa ttttgagagc gttatcaggg cacaataatc 900
116 tcgtcaaatt ctatgatgca tgtgaggatg gcctcaatgt ctacattgtc atggaattat 960
117 gtgagggagg agaattgcta gacagaatat tagccagagg cgggagatac acagaggaag 1020
118 atgccaaagc gattgttgta cagattttga gcgtagtagc cttctgtcat cttcaggggg 1080
119 tagtgcacg tgatttgaag ccagagaatt tccttttcac aaccagggat gaaaatgctc 1140
120 ccatgaagtt gattgatttt ggtctctctg atttcattag accagatgaa aggccttaat 1200
121 atattgttgg aagtgcatat tatgttgcgc cagaggtttt acacagatca tatagtatgg 1260
122 aagcagacat ttggagtata ggtgtcataa cgtacattct gctctgtggc agtcggccat 1320
123 tctgggcacg aacagaatca ggaatattcc gatctgtgtt gagagctgat cccaactttg 1380
124 atgattcacc gtggcctaca gtatcagctg aagctaagga ttttgtgaag agatttctga 1440

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125 acaaagatta cgcacaaaga atgaccgctg ttcaagcact gactcatcct tggttgcgag 1500
126 atgaacaaaag gcagatcccc ctggacatac tcatcttcag attaattaag caatacctcc 1560
127 gcgctacacc tcttaaacgg ttggcattaa aggcaactat caaggcttta agggaagatg 1620
128 aactttttgta tctcaaaactg cagtttaaac tgctcgaacc tagagatggg tttgtatcac 1680
129 ttgacaactt tcggacggca ctaacgcgat atttaactga tgctatgaag gaatcgaggg 1740
130 ttcttgaatt tttgcatgcg ttggaaccac ttgcatacag aagaatggac tttgaagagt 1800
131 tctgtgccgc agcaatcagt ccttaccagc ttgaggcact ggaaagggtg gaggagattg 1860
132 ctggaacagc tttccagcaa ttgacaacag agggcaaccg agtcatatca gttgagggaat 1920
133 tagcacagga attaaatctt gctccaactc attactccat cgttcaagac tggatcagaa 1980
134 aatccgatgg caagctaaac tttctcgggt ttaccaaatt tttacatggt gtcacaataa 2040
135 ggggctcaaa tacaagacgg cattaagcga ttgcaaaaag aaaatgtatt cttttctctt 2100
136 ctaattttta agccgctcat tatgtgaccc tgattgatgt tttcccctcc tgctcctatc 2160
137 cctctggtca atatgatcat tattcttggt cgtgctgctg tcggctggtg tcatcatagt 2220
138 tttttgtaga gaatacatgt aaagatcttt tgtaatgaat cgaatgatat gtttgttcaa 2280
139 gaaatatagt gtcatgttgt tcttttttgc ccagtaaaaa aaaaaaaaaa aaaaatactc 2340
140 gaggcggggc cgtaccacat cccccccctc agcg 2374

```

142 &lt;210&gt; SEQ ID NO: 4

143 &lt;211&gt; LENGTH: 623

144 &lt;212&gt; TYPE: PRT

145 &lt;213&gt; ORGANISM: Oryza sativa

147 &lt;400&gt; SEQUENCE: 4

```

148 Met Gly Gln Cys Tyr Gly Lys Gly Ala Ser Gly Arg Thr Ala Asp Asp
149 1 5 10 15
151 Glu Gly Gly Val Val Thr Glu His Gln Ser Pro Pro Pro Ala Asn Gly
152 20 25 30
154 Leu Pro Ser Thr Pro Pro Arg Gln Gln Ala Gln Ala Gln Ala Gln Gln
155 35 40 45
157 Val Gly Thr Pro Arg Arg Arg Gly Ser Lys Ser Gly Ser Thr Thr Pro
158 50 55 60
160 Gly His Gln Thr Pro Gly Val Ala Trp Pro Ser Pro Tyr Pro Ser Gly
161 65 70 75 80
163 Gly Ala Ser Pro Leu Pro Ala Gly Val Ser Pro Ser Pro Ala Arg Ser
164 85 90 95
166 Thr Pro Arg Arg Phe Phe Lys Arg Pro Phe Pro Pro Pro Ser Pro Ala
167 100 105 110
169 Lys His Ile Lys Ala Thr Leu Ala Lys Arg Leu Gly Gly Gly Lys Pro
170 115 120 125
172 Lys Glu Gly Thr Ile Pro Glu Glu Gly Gly Val Gly Ala Gly Gly Gly
173 130 135 140
175 Gly Gly Gly Ala Ala Asp Gly Ala Glu Thr Glu Arg Pro Leu Asp Lys
176 145 150 155 160
178 Thr Phe Gly Phe Ser Lys Asn Phe Gly Ala Lys Tyr Glu Leu Gly Lys
179 165 170 175
181 Glu Val Gly Arg Gly His Phe Gly His Thr Cys Ser Ala Val Val Lys
182 180 185 190
184 Lys Gly Glu Tyr Lys Gly Gln Thr Val Ala Val Lys Ile Ile Ala Lys
185 195 200 205
187 Ala Lys Met Thr Thr Ala Ile Ser Ile Glu Asp Val Arg Arg Glu Val
188 210 215 220

```

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190 Lys Ile Leu Arg Ala Leu Ser Gly His Asn Asn Leu Val Lys Phe Tyr
191 225      230      235      240
193 Asp Ala Cys Glu Asp Gly Leu Asn Val Tyr Ile Val Met Glu Leu Cys
194      245      250      255
196 Glu Gly Gly Glu Leu Leu Asp Arg Ile Leu Ala Arg Gly Gly Arg Tyr
197      260      265      270
199 Thr Glu Glu Asp Ala Lys Ala Ile Val Val Gln Ile Leu Ser Val Val
200      275      280      285
202 Ala Phe Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro Glu
203      290      295      300
205 Asn Phe Leu Phe Thr Thr Arg Asp Glu Asn Ala Pro Met Lys Leu Ile
206 305      310      315      320
208 Asp Phe Gly Leu Ser Asp Phe Ile Arg Pro Asp Glu Arg Leu Asn Asp
209      325      330      335
211 Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu His Arg Ser
212      340      345      350
214 Tyr Ser Met Glu Ala Asp Ile Trp Ser Ile Gly Val Ile Thr Tyr Ile
215      355      360      365
217 Leu Leu Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr Glu Ser Gly Ile
218      370      375      380
220 Phe Arg Ser Val Leu Arg Ala Asp Pro Asn Phe Asp Asp Ser Pro Trp
221 385      390      395      400
223 Pro Thr Val Ser Ala Glu Ala Lys Asp Phe Val Lys Arg Phe Leu Asn
224      405      410      415
226 Lys Asp Tyr Arg Lys Arg Met Thr Ala Val Gln Ala Leu Thr His Pro
227      420      425      430
229 Trp Leu Arg Asp Glu Gln Arg Gln Ile Pro Leu Asp Ile Leu Ile Phe
230      435      440      445
232 Arg Leu Ile Lys Gln Tyr Leu Arg Ala Thr Pro Leu Lys Arg Leu Ala
233      450      455      460
235 Leu Lys Ala Leu Ser Lys Ala Leu Arg Glu Asp Glu Leu Leu Tyr Leu
236 465      470      475      480
238 Lys Leu Gln Phe Lys Leu Leu Glu Pro Arg Asp Gly Phe Val Ser Leu
239      485      490      495
241 Asp Asn Phe Arg Thr Ala Leu Thr Arg Tyr Leu Thr Asp Ala Met Lys
242      500      505      510
244 Glu Ser Arg Val Leu Glu Phe Leu His Ala Leu Glu Pro Leu Ala Tyr
245      515      520      525
247 Arg Arg Met Asp Phe Glu Glu Phe Cys Ala Ala Ala Ile Ser Pro Tyr
248      530      535      540
250 Gln Leu Glu Ala Leu Glu Arg Trp Glu Glu Ile Ala Gly Thr Ala Phe
251 545      550      555      560
253 Gln Gln Phe Glu Gln Glu Gly Asn Arg Val Ile Ser Val Glu Glu Leu
254      565      570      575
256 Ala Gln Glu Leu Asn Leu Ala Pro Thr His Tyr Ser Ile Val Gln Asp
257      580      585      590
259 Trp Ile Arg Lys Ser Asp Gly Lys Leu Asn Phe Leu Gly Phe Thr Lys
260      595      600      605
262 Phe Leu His Gly Val Thr Ile Arg Gly Ser Asn Thr Arg Arg His

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263      610      615      620
265 <210> SEQ ID NO: 5
266 <211> LENGTH: 568
267 <212> TYPE: DNA
268 <213> ORGANISM: Glycine max
270 <220> FEATURE:
271 <221> NAME/KEY: unsure /
272 <222> LOCATION: (11)
274 <220> FEATURE:
275 <221> NAME/KEY: unsure /
276 <222> LOCATION: (69) /
278 <220> FEATURE: /
279 <221> NAME/KEY: unsure /
280 <222> LOCATION: (83)
282 <220> FEATURE:
283 <221> NAME/KEY: unsure /
284 <222> LOCATION: (95)
286 <220> FEATURE:
287 <221> NAME/KEY: unsure /
288 <222> LOCATION: (148)
290 <220> FEATURE:
291 <221> NAME/KEY: unsure /
292 <222> LOCATION: (196)
294 <220> FEATURE:
295 <221> NAME/KEY: unsure /
296 <222> LOCATION: (272)
298 <220> FEATURE:
299 <221> NAME/KEY: unsure /
300 <222> LOCATION: (557)
302 <220> FEATURE:
303 <221> NAME/KEY: unsure /
304 <222> LOCATION: (563)
306 <220> FEATURE:
307 <221> NAME/KEY: unsure /
308 <222> LOCATION: (568)
310 <400> SEQUENCE: 5
W--> 311 aaacccaagc ncccttccca gctggttcaa aaactcccct tcctcaaact caaacccctag 60
W--> 312 cagcgtcant caacaccctt gcn gatcttc aagcncccct tccctccgcc ctctccggcc 120
W--> 313 aagcacattc gcgcgctgct cgcccgcngc cacggttccg tcaagccgaa cgaagcctcc 180
W--> 314 ataccggagg ccagcnagtg tgagctcggc ctcgacaaga gctttggctt tgctaagcag 240
W--> 315 ttttcggctc attatgagct cagtgcgaa gngggccggg ggcatttttg gtatacctgc 300
316 tccgctaaag gcaagaaagg ggcgttcaag ggcttaaatg ttgctgtcaa agtcattcct 360
317 aaagccaaga tgaccacagc aattgctata gaggatgtaa ggagagaagt gaagatattg 420
318 agggctttaa caggacataa gaatctgggt caattctatg aagcctatga agatgatgac 480
319 atgtttatat agtttgaggt tgtgcaagga gggggaattg ctagatagga ttctttccgg 540
W--> 320 ggtgggaaagt acctcgnaga ggntgcn 568
322 <210> SEQ ID NO: 6
323 <211> LENGTH: 157
324 <212> TYPE: PRT

```

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Input Set : A:\Cpg.pto

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L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:14 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:60 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:61 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1  
L:61 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:83 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2  
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:311 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:312 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:313 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:314 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:314 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:315 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:320 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:356 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:359 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:362 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:365 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:371 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6  
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:404 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7  
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:435 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:438 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8  
L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:629 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:629 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:632 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:634 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:634 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:635 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:635 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:637 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11  
L:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:690 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12

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L:690 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:696 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:696 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:699 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:702 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:708 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12  
L:708 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:765 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:766 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
L:766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:767 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:768 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
L:768 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:852 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14  
L:852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:887 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15  
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15